



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Bb
- (i) APPLICANT: Bonadio, Jeffrey
Yin, Wushan
 - (ii) TITLE OF INVENTION: LATENT TGF(BINDING PROTEIN (LTBP)
GENES, COMPOSITIONS AND METHODS
 - (iii) NUMBER OF SEQUENCES: 13
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Williams, Morgan & Amerson
 - (B) STREET: 7676 Hillmont, Suite 250
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: USA
 - (F) ZIP: 77040
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) -OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/479,722
 - (B) FILING DATE: 07-JUN-1995
 - (C) CLASSIFICATION: Unknown
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US PCT/US95/02251
 - (B) FILING DATE: 21-FEB-1995
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/316,650
 - (B) FILING DATE: 30-SEP-1994
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/199,780
 - (B) FILING DATE: 18-FEB-1994
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fussey, Shelley P.M.
 - (B) REGISTRATION NUMBER: 39,458
 - (C) REFERENCE/DOCKET NUMBER: 4100.000500/FUS
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (713) 934-7000
 - (B) TELEFAX: (713) 934-7011

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5499 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..5499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	GAG	AGC	ACC	TCC	CCG	CGA	GGT	CTC	CGG	TGC	CCA	CAG	CTC	TGC	AGC	48
Met	Glu	Ser	Thr	Ser	Pro	Arg	Gly	Leu	Arg	Cys	Pro	Gln	Leu	Cys	Ser	
1				5				10						15		
CAC	TCT	GGC	GCC	ATG	AGA	GCG	CCG	ACC	ACC	GCT	CGC	TGC	TCC	GGA	TGC	96
His	Ser	Gly	Ala	Met	Arg	Ala	Pro	Thr	Thr	Ala	Arg	Cys	Ser	Gly	Cys	
			20					25					30			
ATC	CAA	CGG	GTG	CGT	TGG	AGG	GGC	TTC	CTG	CCA	CTT	GTC	CTG	GCT	GTC	144
Ile	Gln	Arg	Val	Arg	Trp	Arg	Gly	Phe	Leu	Pro	Leu	Val	Leu	Ala	Val	
		35					40					45				
TTG	ATG	GGG	ACA	AGT	CAT	GCC	CAA	CGG	GAT	TCC	ATA	GGG	AGA	TAC	GAA	192
Leu	Met	Gly	Thr	Ser	His	Ala	Gln	Arg	Asp	Ser	Ile	Gly	Arg	Tyr	Glu	
	50					55					60					
CCA	GCT	AGC	AGG	GAT	GCG	AAT	CGG	TTG	TGG	CAC	CCC	GTG	GGC	AGC	CAC	240
Pro	Ala	Ser	Arg	Asp	Ala	Asn	Arg	Leu	Trp	His	Pro	Val	Gly	Ser	His	
65					70					75					80	
CCC	GCA	GCG	GCT	GCA	GCC	AAG	GTG	TAC	AGT	CTG	TTC	CGA	GAG	CCT	GAC	288
Pro	Ala	Ala	Ala	Ala	Ala	Lys	Val	Tyr	Ser	Leu	Phe	Arg	Glu	Pro	Asp	
				85				90						95		
GCG	CCG	GTC	CCC	GGC	TTG	TCG	CCC	TCT	GAG	TGG	AAC	CAG	CCG	GCC	CAG	336
Ala	Pro	Val	Pro	Gly	Leu	Ser	Pro	Ser	Glu	Trp	Asn	Gln	Pro	Ala	Gln	
			100					105					110			
GGG	AAC	CCG	GGA	TGG	CTC	GCA	GAG	GCC	GAG	GCC	AGG	AGG	CCA	CCT	CGA	384
Gly	Asn	Pro	Gly	Trp	Leu	Ala	Glu	Ala	Glu	Ala	Arg	Arg	Pro	Pro	Arg	
	115					120					125					
ACC	CAG	CAG	CTG	CGT	CGA	GTC	CAG	CCA	CCT	GTC	CAG	ACT	CGG	AGA	AGC	432
Thr	Gln	Gln	Leu	Arg	Arg	Val	Gln	Pro	Pro	Val	Gln	Thr	Arg	Arg	Ser	
	130					135					140					
CAT	CCC	CGG	GGC	CAG	CAG	CAG	ATA	GCA	GCC	CGG	GCT	GCA	CCT	TCT	GTC	480
His	Pro	Arg	Gly	Gln	Gln	Gln	Ile	Ala	Ala	Arg	Ala	Ala	Pro	Ser	Val	
145					150					155					160	
GCG	CGC	CTG	GAA	ACC	CCT	CAG	CGA	CCC	GCG	GCT	GCA	CGG	CGA	GGG	CGG	528
Ala	Arg	Leu	Glu	Thr	Pro	Gln	Arg	Pro	Ala	Ala	Ala	Arg	Arg	Gly	Arg	
			165					170						175		
CTC	ACT	GGG	AGA	AAT	GTC	TGC	GGG	GGA	CAG	TGC	TGC	CCA	GGA	TGG	ACA	576

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Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly Trp Thr	
180 185 190	
ACA TCA AAC AGC ACC AAC CAC TGT ATC AAA CCT GTG TGT CAG CCT CCC	624
Thr Ser Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Gln Pro Pro	
195 200 205	
TGT CAG AAC CGA GGC TCC TGC AGC AGG CCC CAG GTC TGC ATC TGC CGT	672
Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Val Cys Ile Cys Arg	
210 215 220	
TCT GGC TTC CGT JGG GCG CGC TGT GAG GAG GTC ATC CCT GAG GAG GAA	720
Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Glu Glu Glu	
225 230 235 240	
TTT GAC CCT CAG AAT GCC AGG CCT GTG CCC AGA CGC TCA GTG GAG AGA	768
Phe Asp Pro Gln Asn Ala Arg Pro Val Pro Arg Arg Ser Val Glu Arg	
245 250 255	
GCA CCC GGT CCT CAC AGA AGC AGT GAG GCC AGA GGA AGT CTA GTG ACC	816
Ala Pro Gly Pro His Arg Ser Ser Glu Ala Arg Gly Ser Leu Val Thr	
260 265 270	
AGA ATA CAG CCG CTG GTA CCA CCA CCA TCA CCA CCT CCA TCT CGG CGC	864
Arg Ile Gln Pro Leu Val Pro Pro Pro Ser Pro Pro Ser Arg Arg	
275 280 285	
CTC AGC CAG CCC TGG CCC CTG CAG CAG CAC TCA GGG CCG TCC AGG ACA	912
Leu Ser Gln Pro Trp Pro Leu Gln Gln His Ser Gly Pro Ser Arg Thr	
290 295 300	
GTT CGT CGG TAT CCG GCC ACT GGT GCC AAT GGC CAG CTG ATG TCC AAC	960
Val Arg Arg Tyr Pro Ala Thr Gly Ala Asn Gly Gln Leu Met Ser Asn	
305 310 315 320	
GCT TTG CCT TCA GGA CTC GAG CTG AGA GAC AGC AGC CCA CAG GCA GCA	1008
Ala Leu Pro Ser Gly Leu Glu Leu Arg Asp Ser Ser Pro Gln Ala Ala	
325 330 335	
CAT GTG AAC CAT CTC TCA CCC CCC TGG GGG CTG AAC CTC ACC GAG AAA	1056
His Val Asn His Leu Ser Pro Pro Trp Gly Leu Asn Leu Thr Glu Lys	
340 345 350	
ATC AAG AAA ATC AAA GTC GTC TTC ACC CCC ACC ATC TGC AAG CAG ACC	1104
Ile Lys Lys Ile Lys Val Val Phe Thr Pro Thr Ile Cys Lys Gln Thr	
355 360 365	
TGT GCC CGG GGA CGC TGT GCC AAC AGC TGT GAG AAG GGT GAC ACC ACC	1152
Cys Ala Arg Gly Arg Cys Ala Asn Ser Cys Glu Lys Gly Asp Thr Thr	
370 375 380	
ACC TTG TAC AGT CAG GGT GGC CAT GGG CAT GAC CCC AAG TCT GGC TTC	1200
Thr Leu Tyr Ser Gln Gly Gly His Gly His Asp Pro Lys Ser Gly Phe	
385 390 395 400	
CGT ATC TAT TTC TGC CAA ATC CCC TGC CTG AAT GGT GGC CGC TGC ATC	1248
Arg Ile Tyr Phe Cys Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile	

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405										410					415					
GGC	CGG	GAC	GAG	TGC	TGG	TGT	CCA	GCC	AAC	TCC	ACA	GGA	AAG	TTC	TGC	1296				
Gly	Arg	Asp	Glu	Cys	Trp	Cys	Pro	Ala	Asn	Ser	Thr	Gly	Lys	Phe	Cys					
			420				425				430									
CAT	CTG	CCT	GTC	CCG	CAG	CCA	GAC	AGG	GAA	CCT	GCA	GGG	CGA	GGT	TCC	1344				
His	Leu	Pro	Val	Pro	Gln	Pro	Asp	Arg	Glu	Pro	Ala	Gly	Arg	Gly	Ser					
			435				440				445									
CGG	CAC	AGA	ACC	CTG	CTG	GAA	GGT	CCC	CTG	AAG	CAA	TCC	ACC	TTC	ACG	1392				
Arg	His	Arg	Thr	Leu	Leu	Glu	Gly	Pro	Leu	Lys	Gln	Ser	Thr	Phe	Thr					
			450				455				460									
CTG	CCT	CTC	TCT	AAC	CAG	CTC	GCC	TCT	GTG	AAC	CCC	TCG	CTG	GTG	AAG	1440				
Leu	Pro	Leu	Ser	Asn	Gln	Leu	Ala	Ser	Val	Asn	Pro	Ser	Leu	Val	Lys					
			465				470				475				480					
GTG	CAA	ATT	CAT	CAC	CCG	CCT	GAG	GCC	TCT	GTG	CAG	ATT	CAC	CAG	GTG	1488				
Val	Gln	Ile	His	His	Pro	Pro	Glu	Ala	Ser	Val	Gln	Ile	His	Gln	Val					
			485				490				495									
GCC	CGG	GTC	CGG	GGT	GAG	CTG	GAC	CCC	GTG	CTG	GAG	GAC	AAC	AGT	GTG	1536				
Ala	Arg	Val	Arg	Gly	Glu	Leu	Asp	Pro	Val	Leu	Glu	Asp	Asn	Ser	Val					
			500				505				510									
GAG	ACC	AGA	GCC	TCT	CAT	CGC	CCC	CAC	GGC	AAC	CTA	GGC	CAC	AGC	CCC	1584				
Glu	Thr	Arg	Ala	Ser	His	Arg	Pro	His	Gly	Asn	Leu	Gly	His	Ser	Pro					
			515				520				525									
TGG	GCC	AGC	AAC	AGC	ATA	CCC	GCT	CGG	GCC	GGA	GAG	GCC	CCT	CGG	CCA	1632				
Trp	Ala	Ser	Asn	Ser	Ile	Pro	Ala	Arg	Ala	Gly	Glu	Ala	Pro	Arg	Pro					
			530				535				540									
CCA	CCA	GTG	CTG	TCT	AGG	CAT	TAT	GGA	CTT	CTC	GGC	CAG	TGT	TAC	CTG	1680				
Pro	Pro	Val	Leu	Ser	Arg	His	Tyr	Gly	Leu	Leu	Gly	Gln	Cys	Tyr	Leu					
			545				550				555				560					
AGC	ACG	GTG	AAT	GGA	CAG	TGT	GCT	AAC	CCC	CTA	GGT	AGT	CTG	ACT	TCT	1728				
Ser	Thr	Val	Asn	Gly	Gln	Cys	Ala	Asn	Pro	Leu	Gly	Ser	Leu	Thr	Ser					
			565				570				575									
CAG	GAG	GAC	TGC	TGT	GGC	AGT	GTG	GGG	ACC	TTC	TGG	GGG	GTG	ACC	TCC	1776				
Gln	Glu	Asp	Cys	Cys	Gly	Ser	Val	Gly	Thr	Phe	Trp	Gly	Val	Thr	Ser					
			580				585				590									
TGT	GCT	CCC	TGC	CCA	CCC	AGA	CAA	GAG	GGT	CCA	GCC	TTC	CCA	GTG	ATT	1824				
Cys	Ala	Pro	Cys	Pro	Pro	Arg	Gln	Glu	Gly	Pro	Ala	Phe	Pro	Val	Ile					
			595				600				605									
GAA	AAT	GGC	CAG	CTG	GAG	TGT	CCC	CAA	GGA	TAC	AAG	AGA	CTG	AAC	CTC	1872				
Glu	Asn	Gly	Gln	Leu	Glu	Cys	Pro	Gln	Gly	Tyr	Lys	Arg	Leu	Asn	Leu					
			610				615				620									
AGC	CAC	TGC	CAA	GAT	ATC	AAT	GAG	TGC	CTG	ACC	CTG	GGC	CTC	TGC	AAG	1920				
Ser	His	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Leu	Gly	Leu	Cys	Lys					
			625				630				635				640					

GAC TCG GAG TGC GTG AAC ACC AGG GGC AGC TAC CTG TGC ACC TGC AGG	1968
Asp Ser Glu Cys Val Asn Thr Arg Gly Ser Tyr Leu Cys Thr Cys Arg	
645 650 655	
CCT GGC CTC ATG CTG GAT CCG TCA AGG AGC CGC TGC GTA TCG GAC AAG	2016
Pro Gly Leu Met Leu Asp Pro Ser Arg Ser Arg Cys Val Ser Asp Lys	
660 665 670	
GCT GTC TCC ATG CAG CAG GGA CTA TGC TAC CGG TCA CTG GGG TCT GGT	2064
Ala Val Ser Met Gln Gln Gly Leu Cys Tyr Arg Ser Leu Gly Ser Gly	
675 680 685	
ACC TGC ACC CTG CCT TTG GTT CAT CGG ATC ACC AAG CAG ATA TGC TGC	2112
Thr Cys Thr Leu Pro Leu Val His Arg Ile Thr Lys Gln Ile Cys Cys	
690 695 700	
TGC AGC CGT GTG GGC AAA GCC TGG GGT AGC ACA TGT GAA CAG TGT CCC	2160
Cys Ser Arg Val Gly Lys Ala Trp Gly Ser Thr Cys Glu Gln Cys Pro	
705 710 715 720	
CTG CCT GGC ACA GAA GCC TTC AGG GAG ATC TGC CCT GCT GGC CAT GGC	2208
Leu Pro Gly Thr Glu Ala Phe Arg Glu Ile Cys Pro Ala Gly His Gly	
725 730 735	
TAC ACC TAC TCG AGC TCA GAC ATC CGC CTG TCT ATG AGG AAA GCC GAA	2256
Tyr Thr Tyr Ser Ser Ser Asp Ile Arg Leu Ser Met Arg Lys Ala Glu	
740 745 750	
GAA GAG GAA CTG GCT AGC CCC TTA AGG GAG CAG ACA GAG CAG AGC ACT	2304
Glu Glu Glu Leu Ala Ser Pro Leu Arg Glu Gln Thr Glu Gln Ser Thr	
755 760 765	
GCA CCC CCA CCT GGG CAA GCA GAG AGG CAA CCA CTC CGG GCA GCC ACC	2352
Ala Pro Pro Pro Gly Gln Ala Glu Arg Gln Pro Leu Arg Ala Ala Thr	
770 775 780	
GCC ACC TGG ATT GAG GCT GAG ACC CTC CCT GAC AAA GGT GAC TCT CGG	2400
Ala Thr Trp Ile Glu Ala Glu Thr Leu Pro Asp Lys Gly Asp Ser Arg	
785 790 795 800	
GCT GTT CAG ATC ACA ACC AGT GCT CCC CAC CTA CCT GCC CGG GTA CCA	2448
Ala Val Gln Ile Thr Thr Ser Ala Pro His Leu Pro Ala Arg Val Pro	
805 810 815	
GGG GAT GCC ACT GGA AGA CCA GCA CCA TCC TTG CCT GGA CAG GGC ATT	2496
Gly Asp Ala Thr Gly Arg Pro Ala Pro Ser Leu Pro Gly Gln Gly Ile	
820 825 830	
CCA GAG AGT CCA GCA GAA GAG CAA GTG ATT CCC TCC AGT GAT GTC TTG	2544
Pro Glu Ser Pro Ala Glu Glu Gln Val Ile Pro Ser Ser Asp Val Leu	
835 840 845	
GTG ACA CAC AGC CCC CCA GAC TTT GAT CCA TGT TTT GCT GGA GCC TCC	2592
Val Thr His Ser Pro Pro Asp Phe Asp Pro Cys Phe Ala Gly Ala Ser	
850 855 860	

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AAC ATC TGT GGC CCT GGG ACC TGT GTG AGC CTC CCA AAT GGA TAC AGA Asn Ile Cys Gly Pro Gly Thr Cys Val Ser Leu Pro Asn Gly Tyr Arg 865 870 875 880	2640
TGT GTC TGC AGC CCT GGC TAC CAG CTA CAC CCC AGC CAA GAC TAC TGT Cys Val Cys Ser Pro Gly Tyr Gln Leu His Pro Ser Gln Asp Tyr Cys 885 890 895	2688
ACT GAT GAC AAC GAG TGT ATG AGG AAC CCC TGT GAA GGA AGA GGG CGC Thr Asp Asp Asn Glu Cys Met Arg Asn Pro Cys Glu Gly Arg Gly Arg 900 905 910	2736
TGT GTC AAC AGT GTG GGC TCC TAC TCC TGC CTC TGC TAT CCT GGC TAC Cys Val Asn Ser Val Gly Ser Tyr Ser Cys Leu Cys Tyr Pro Gly Tyr 915 920 925	2784
ACA CTA GTC ACC CTC GGA GAC ACA CAG GAG TGC CAA GAT ATC GAT GAG Thr Leu Val Thr Leu Gly Asp Thr Gln Glu Cys Gln Asp Ile Asp Glu 930 935 940	2832
TGT GAG CAG CCC GGG GTG TGC AGT GGT GGG CGA TGC AGC AAC ACG GAG Cys Glu Gln Pro Gly Val Cys Ser Gly Gly Arg Cys Ser Asn Thr Glu 945 950 955 960	2880
GGC TCG TAC CAC TGC GAG TGT GAT CGG GGC TAC ATC ATG GTC AGG AAA Gly Ser Tyr His Cys Glu Cys Asp Arg Gly Tyr Ile Met Val Arg Lys 965 970 975	2928
GGA CAC TGT CAA GAT ATC AAC GAA TGC CGT CAC CCT GGT ACC TGC CCT Gly His Cys Gln Asp Ile Asn Glu Cys Arg His Pro Gly Thr Cys Pro 980 985 990	2976
GAT GGG AGA TGC GTC AAC TCC CCT GGC TCC TAC ACT TGT CTG GCC TGT Asp Gly Arg Cys Val Asn Ser Pro Gly Ser Tyr Thr Cys Leu Ala Cys 995 1000 1005	3024
GAG GAG GGC TAT GTA GGC CAG AGT GGG AGC TGT GTA GAT GTC AAT GAG Glu Glu Gly Tyr Val Gly Gln Ser Gly Ser Cys Val Asp Val Asn Glu 1010 1015 1020	3072
TGT CTG ACC CCT GGG ATA TGT ACC CAT GGA AGG TGC ATC AAC ATG GAA Cys Leu Thr Pro Gly Ile Cys Thr His Gly Arg Cys Ile Asn Met Glu 1025 1030 1035 1040	3120
GGC TCC TTT AGA TGC TCC TGT GAG CCG GGC TAT GAG GTC ACC CCA GAC Gly Ser Phe Arg Cys Ser Cys Glu Pro Gly Tyr Glu Val Thr Pro Asp 1045 1050 1055	3168
AAG AAG GGC TGC CGA GAT GTG GAC GAG TGT GCC AGC CGA GCC TCG TGC Lys Lys Gly Cys Arg Asp Val Asp Glu Cys Ala Ser Arg Ala Ser Cys 1060 1065 1070	3216
CCC ACG GGC CTC TGC CTC AAC ACG GAG GGC TCC TTC ACC TGC TCA GCC Pro Thr Gly Leu Cys Leu Asn Thr Glu Gly Ser Phe Thr Cys Ser Ala 1075 1080 1085	3264
TGT CAG AGC GGG TAC TGG GTG AAC GAA GAT GGC ACT GCC TGT GAA GAC	3312

Cys Gln Ser Gly Tyr Trp Val Asn Glu Asp Gly Thr Ala Cys Glu Asp	
1090 1095 1100	
TTG GAT GAA TGT GCC TTC CCT GGA GTC TGC CCC ACA GGC GTC TGC ACC	3360
Leu Asp Glu Cys Ala Phe Pro Gly Val Cys Pro Thr Gly Val Cys Thr	
1105 1110 1115 1120	
AAT ACT GTA GGC TCC TTC TCC TGC AAG GAC TGT GAC CAG GGC TAC CGG	3408
Asn Thr Val Gly Ser Phe Ser Cys Lys Asp Cys Asp Gln Gly Tyr Arg	
1125 1130 1135	
CCC AAC CCC CTG GGC AAC AGA TGC GAA GAT GTG GAT GAG TGT GAA GGT	3456
Pro Asn Pro Leu Gly Asn Arg Cys Glu Asp Val Asn Glu Cys Glu Gly	
1140 1145 1150	
CCC CAA AGC AGC TGC CGG GGA GGC GAA TGC AAG AAC ACA GAA GGT TCC	3504
Pro Gln Ser Ser Cys Arg Gly Gly Glu Cys Lys Asn Thr Glu Gly Ser	
1155 1160 1165	
TAC CAA TGC CTC TGT CAC CAG GGC TTC CAG CTG GTC AAT GGC ACC ATG	3552
Tyr Gln Cys Leu Cys His Gln Gly Phe Gln Leu Val Asn Gly Thr Met	
1170 1175 1180	
TGT GAG GAC GTG AAT GAG TGT GTT GGG GAA GAG CAT TGT GCT CCT CAC	3600
Cys Glu Asp Val Asn Glu Cys Val Gly Glu Glu His Cys Ala Pro His	
1185 1190 1195 1200	
GGC GAG TGC CTC AAC AGC CTG GGC TCC TTC TTC TGC CTC TGT GCA CCC	3648
Gly Glu Cys Leu Asn Ser Leu Gly Ser Phe Phe Cys Leu Cys Ala Pro	
1205 1210 1215	
GGC TTT GCT AGT GCT GAG GGG GGC ACC AGA TGC CAG GAT GTT GAT GAA	3696
Gly Phe Ala Ser Ala Glu Gly Gly Thr Arg Cys Gln Asp Val Asp Glu	
1220 1225 1230	
TGT GCA GCC ACA GAC CCG TGT CCG GGA GGA CAC TGT GTC AAC ACA GAG	3744
Cys Ala Ala Thr Asp Pro Cys Pro Gly Gly His Cys Val Asn Thr Glu	
1235 1240 1245	
GGC TCC TTC AGC TGT CTG TGT GAG ACT GCT TCC TTC CAG CCC TCC CCA	3792
Gly Ser Phe Ser Cys Leu Cys Glu Thr Ala Ser Phe Gln Pro Ser Pro	
1250 1255 1260	
GAC AGC GGA GAA TGT TTG GAT ATT GAT GAG TGT GAG GAC CGT GAA GAC	3840
Asp Ser Gly Glu Cys Leu Asp Ile Asp Glu Cys Glu Asp Arg Glu Asp	
1265 1270 1275 1280	
CCG GTG TGC GGA GCC TGG AGG TGT GAG AAC AGT CCT GGT TCC TAC CGC	3888
Pro Val Cys Gly Ala Trp Arg Cys Glu Asn Ser Pro Gly Ser Tyr Arg	
1285 1290 1295	
TGC ATC CTG GAC TGC CAG CCT GGA TTC TAT GTG GCG CCA AAT GGA GAC	3936
Cys Ile Leu Asp Cys Gln Pro Gly Phe Tyr Val Ala Pro Asn Gly Asp	
1300 1305 1310	
TGC ATT GAC ATA GAT GAA TGT GCC AAT GAC ACT GTG TGT GGG AAC CAT	3984
Cys Ile Asp Ile Asp Glu Cys Ala Asn Asp Thr Val Cys Gly Asn His	

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1315	1320	1325	
GGC TTC TGT GAC AAC ACG GAC Gly Phe Cys Asp Asn Thr Asp 1330	GGC TCC TTC CGC TGC CTG TGT GAC CAG Gly Ser Phe Arg Cys Leu Cys Asp Gln 1335		4032
GGC TTC GAG ACC TCA CCA TCA GGC TGG GAG TGT GTT GAT GTG AAC GAG Gly Phe Glu Thr Ser Pro Ser Gly Trp Glu Cys Val Asp Val Asn Glu 1345		1355	4080
TGT GAG CTC ATG ATG GCA GTG TGT GGG GAT GCG CTC TGT GAG AAC GTG Cys Glu Leu Met Met Ala Val Cys Gly Asp Ala Leu Cys Glu Asn Val 1365		1370	4128
GAA GGC TCC TTC CTG TGC CTT TGC GCC AGT GAC CTT GAG GAG TAC GAC Glu Gly Ser Phe Leu Cys Leu Cys Ala Ser Asp Leu Glu Glu Tyr Asp 1380		1385	4176
GCA GAA GAA GGA CAC TGC CGT CCT CGG GTG GCT GGA GCT CAG AGA ATC Ala Glu Glu Gly His Cys Arg Pro Arg Val Ala Gly Ala Gln Arg Ile 1395		1400	4224
CCA GAG GTC CGG ACA GAG GAC CAG GCT CCA AGC CTT ATC CGC ATG GAA Pro Glu Val Arg Thr Glu Asp Gln Ala Pro Ser Leu Ile Arg Met Glu 1410		1415	4272
TGC TAC TCT GAA CAC AAT GGT GGT CCT CCC TGC TCT CAA ATC CTG GGC Cys Tyr Ser Glu His Asn Gly Gly Pro Pro Cys Ser Gln Ile Leu Gly 1425		1430	4320
CAG AAC TCC ACA CAG GCC GAG TGC TGC TGC ACT CAG GGT GCC AGA TGG Gln Asn Ser Thr Gln Ala Glu Cys Cys Cys Thr Gln Gly Ala Arg Trp 1445		1450	4368
GGA AAG GCC TGT GCG CCC TGC CCA TCT GAG GAC TCA GTT GAA TTC AGT Gly Lys Ala Cys Ala Pro Cys Pro Ser Glu Asp Ser Val Glu Phe Ser 1460		1465	4416
CAG CTC TGC CCC AGT GGT CAA GGT TAC ATC CCA GTG GAA GGA GCC TGG Gln Leu Cys Pro Ser Gly Gln Gly Tyr Ile Pro Val Glu Gly Ala Trp 1475		1480	4464
ACA TTT GGA CAA ACC ATG TAT ACA GAT GCC GAT GAA TGT GTA CTG TTT Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu Cys Val Leu Phe 1490		1495	4512
GGG CCT GCT CTC TGC CAG AAT GGC CGA TGC TCA AAC ATA GTG CCT GGC Gly Pro Ala Leu Cys Gln Asn Gly Arg Cys Ser Asn Ile Val Pro Gly 1505		1510	4560
TAC ATT TGC CTG TGC AAC CCT GGC TAC CAC TAT GAT GCC TCC AGC AGG Tyr Ile Cys Leu Cys Asn Pro Gly Tyr His Tyr Asp Ala Ser Ser Arg 1525		1530	4608
AAG TGC CAG GAT CAC AAC GAA TGC CAG GAC TTG GCC TGT GAG AAC GGT Lys Cys Gln Asp His Asn Glu Cys Gln Asp Leu Ala Cys Glu Asn Gly 1540		1545	4656

GAG TGT GTG AAC CAA GAA GGC TCC TTC CAT TGC CTC TGC AAT CCC CCC Glu Cys Val Asn Gln Glu Gly Ser Phe His Cys Leu Cys Asn Pro Pro 1555 1560 1565	4704
CTC ACC CTA GAC CTC AGT GGG CAG CGC TGT GTG AAC ACG ACC AGC AGC Leu Thr Leu Asp Leu Ser Gly Gln Arg Cys Val Asn Thr Thr Ser Ser 1570 1575 1580	4752
ACG GAG GAC TTC CCT GAC CAT GAC ATC CAC ATG GAC ATC TGC TGG AAA Thr Glu Asp Phe Pro Asp His Asp Ile His Met Asp Ile Cys Trp Lys 1585 1590 1595 1600	4800
AAA GTC ACC AAT GAT GTG TGC AGC CAG CCC TTG CGT GGG CAC CAT ACC Lys Val Thr Asn Asp Val Cys Ser Gln Pro Leu Arg Gly His His Thr 1605 1610 1615	4848
ACC TAT ACA GAA TGC TGC TGC CAA GAT GGG GAG GCC TGG AGC CAG CAA Thr Tyr Thr Glu Cys Cys Cys Gln Asp Gly Glu Ala Trp Ser Gln Gln 1620 1625 1630	4896
TGC GCT CTG TGC CCG CCC AGG AGC TCT GAG GTC TAC GCT CAG CTG TGC Cys Ala Leu Cys Pro Pro Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys 1635 1640 1645	4944
AAC GTG GCT CGG ATT GAG GCA GAG CGC GGA GCA GGG ATC CAC TTC CGG Asn Val Ala Arg Ile Glu Ala Glu Arg Gly Ala Gly Ile His Phe Arg 1650 1655 1660	4992
CCA GGC TAT GAG TAT GGC CCT GGC CTG GAC GAT CTG CCT GAA AAC CTC Pro Gly Tyr Glu Tyr Gly Pro Gly Leu Asp Asp Leu Pro Glu Asn Leu 1665 1670 1675 1680	5040
TAC GGC CCA GAT GGG GCT CCC TTC TAT AAC TAC CTA GGC CCC GAG GAC Tyr Gly Pro Asp Gly Ala Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp 1685 1690 1695	5088
ACT GCC CCT GAG CCT CCC TTC TCC AAC CCA GCC AGC CAG CCG GGA GAC Thr Ala Pro Glu Pro Pro Phe Ser Asn Pro Ala Ser Gln Pro Gly Asp 1700 1705 1710	5136
AAC ACA CCT GTC CTT GAG CCT CCT CTG CAG CCC TCT GAA CTT CAG CCT Asn Thr Pro Val Leu Glu Pro Pro Leu Gln Pro Ser Glu Leu Gln Pro 1715 1720 1725	5184
CAC TAT CTA GCC AGC CAC TCA GAA CCC CCT GCC TCC TTC GAA GGC CTT His Tyr Leu Ala Ser His Ser Glu Pro Pro Ala Ser Phe Glu Gly Leu 1730 1735 1740	5232
CAG GCT GAG GAA TGT GGC ATC CTG AAT GGC TGT GAG AAT GGC CGC TGC Gln Ala Glu Glu Cys Gly Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys 1745 1750 1755 1760	5280
GTG CGT GTG CGG GAG GGC TAC ACT TGC GAC TGC TTT GAG GGC TTC CAG Val Arg Val Arg Glu Gly Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln 1765 1770 1775	5328

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CTG GAT GCG CCC ACA TTG GCC TGT GTG GAT GTG AAC GAG TGT GAA GAC 5376
 Leu Asp Ala Pro Thr Leu Ala Cys Val Asp Val Asn Glu Cys Glu Asp
 1780 1785 1790

TTG AAC GGG CCT GCA CGA CTC TGT GCA CAC GGT CAC TGT GAG AAC ACA 5424
 Leu Asn Gly Pro Ala Arg Leu Cys Ala His Gly His Cys Glu Asn Thr
 1795 1800 1805

GAG GGT TCC TAT CGC TGC CAC TGT TCG CCA GGT TAC GTG GCA GAG CCA 5472
 Glu Gly Ser Thr Arg Cys His Cys Ser Pro Gly Tyr Val Ala Glu Pro
 1810 1815 1820

GGC CCC CCA CAC TGT GCG GCC AAG GAG 5499
 Gly Pro Pro His Cys Ala Ala Lys Glu
 1825 1830

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1833 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Thr Ser Pro Arg Gly Leu Arg Cys Pro Gln Leu Cys Ser
 1 5 10 15

His Ser Gly Ala Met Arg Ala Pro Thr Thr Ala Arg Cys Ser Gly Cys
 20 25 30

Ile Gln Arg Val Arg Trp Arg Gly Phe Leu Pro Leu Val Leu Ala Val
 35 40 45

Leu Met Gly Thr Ser His Ala Gln Arg Asp Ser Ile Gly Arg Tyr Glu
 50 55 60

Pro Ala Ser Arg Asp Ala Asn Arg Leu Trp His Pro Val Gly Ser His
 65 70 75 80

Pro Ala Ala Ala Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Pro Asp
 85 90 95

Ala Pro Val Pro Gly Leu Ser Pro Ser Glu Trp Asn Gln Pro Ala Gln
 100 105 110

Gly Asn Pro Gly Trp Leu Ala Glu Ala Glu Ala Arg Arg Pro Pro Arg
 115 120 125

Thr Gln Gln Leu Arg Arg Val Gln Pro Pro Val Gln Thr Arg Arg Ser
 130 135 140

His Pro Arg Gly Gln Gln Gln Ile Ala Ala Arg Ala Ala Pro Ser Val
 145 150 155 160

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Ala Arg Leu Glu Thr Pro Gln Arg Pro Ala Ala Ala Arg Arg Gly Arg
165 170 175

Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly Trp Thr
180 185 190

Thr Ser Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Gln Pro Pro
195 200 205

Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Val Cys Ile Cys Arg
210 215 220

Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Glu Glu Glu
225 230 235 240

Phe Asp Pro Gln Asn Ala Arg Pro Val Pro Arg Arg Ser Val Glu Arg
245 250 255

Ala Pro Gly Pro His Arg Ser Ser Glu Ala Arg Gly Ser Leu Val Thr
260 265 270

Arg Ile Gln Pro Leu Val Pro Pro Pro Ser Pro Pro Ser Arg Arg
275 280 285

Leu Ser Gln Pro Trp Pro Leu Gln Gln His Ser Gly Pro Ser Arg Thr
290 295 300

Val Arg Arg Tyr Pro Ala Thr Gly Ala Asn Gly Gln Leu Met Ser Asn
305 310 315 320

Ala Leu Pro Ser Gly Leu Glu Leu Arg Asp Ser Ser Pro Gln Ala Ala
325 330 335

His Val Asn His Leu Ser Pro Pro Trp Gly Leu Asn Leu Thr Glu Lys
340 345 350

Ile Lys Lys Ile Lys Val Val Phe Thr Pro Thr Ile Cys Lys Gln Thr
355 360 365

Cys Ala Arg Gly Arg Cys Ala Asn Ser Cys Glu Lys Gly Asp Thr Thr
370 375 380

Thr Leu Tyr Ser Gln Gly Gly His Gly His Asp Pro Lys Ser Gly Phe
385 390 395 400

Arg Ile Tyr Phe Cys Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile
405 410 415

Gly Arg Asp Glu Cys Trp Cys Pro Ala Asn Ser Thr Gly Lys Phe Cys
420 425 430

His Leu Pro Val Pro Gln Pro Asp Arg Glu Pro Ala Gly Arg Gly Ser
435 440 445

Arg His Arg Thr Leu Leu Glu Gly Pro Leu Lys Gln Ser Thr Phe Thr
450 455 460

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Leu	Pro	Leu	Ser	Asn	Gln	Leu	Ala	Ser	Val	Asn	Pro	Ser	Leu	Val	Lys	465	470	475	480
Val	Gln	Ile	His	His	Pro	Pro	Glu	Ala	Ser	Val	Gln	Ile	His	Gln	Val	485	490	495	
Ala	Arg	Val	Arg	Gly	Glu	Leu	Asp	Pro	Val	Leu	Glu	Asp	Asn	Ser	Val	500	505	510	
Glu	Thr	Arg	Ala	Ser	His	Arg	Pro	His	Gly	Asn	Leu	Gly	His	Ser	Pro	515	520	525	
Trp	Ala	Ser	Asn	Ser	Ile	Pro	Ala	Arg	Ala	Gly	Glu	Ala	Pro	Arg	Pro	530	535	540	
Pro	Pro	Val	Leu	Ser	Arg	His	Tyr	Gly	Leu	Leu	Gly	Gln	Cys	Tyr	Leu	545	550	555	560
Ser	Thr	Val	Asn	Gly	Gln	Cys	Ala	Asn	Pro	Leu	Gly	Ser	Leu	Thr	Ser	565	570	575	
Gln	Glu	Asp	Cys	Cys	Gly	Ser	Val	Gly	Thr	Phe	Trp	Gly	Val	Thr	Ser	580	585	590	
Cys	Ala	Pro	Cys	Pro	Pro	Arg	Gln	Glu	Gly	Pro	Ala	Phe	Pro	Val	Ile	595	600	605	
Glu	Asn	Gly	Gln	Leu	Glu	Cys	Pro	Gln	Gly	Tyr	Lys	Arg	Leu	Asn	Leu	610	615	620	
Ser	His	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Leu	Thr	Leu	Gly	Leu	Cys	Lys	625	630	635	640
Asp	Ser	Glu	Cys	Val	Asn	Thr	Arg	Gly	Ser	Tyr	Leu	Cys	Thr	Cys	Arg	645	650	655	
Pro	Gly	Leu	Met	Leu	Asp	Pro	Ser	Arg	Ser	Arg	Cys	Val	Ser	Asp	Lys	660	665	670	
Ala	Val	Ser	Met	Gln	Gln	Gly	Leu	Cys	Tyr	Arg	Ser	Leu	Gly	Ser	Gly	675	680	685	
Thr	Cys	Thr	Leu	Pro	Leu	Val	His	Arg	Ile	Thr	Lys	Gln	Ile	Cys	Cys	690	695	700	
Cys	Ser	Arg	Val	Gly	Lys	Ala	Trp	Gly	Ser	Thr	Cys	Glu	Gln	Cys	Pro	705	710	715	720
Leu	Pro	Gly	Thr	Glu	Ala	Phe	Arg	Glu	Ile	Cys	Pro	Ala	Gly	His	Gly	725	730	735	
Tyr	Thr	Tyr	Ser	Ser	Ser	Asp	Ile	Arg	Leu	Ser	Met	Arg	Lys	Ala	Glu	740	745	750	
Glu	Glu	Glu	Leu	Ala	Ser	Pro	Leu	Arg	Glu	Gln	Thr	Glu	Gln	Ser	Thr	755	760	765	

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Lys Lys Gly Cys Arg Asp Val Asp Glu Cys Ala Ser Arg Ala Ser Cy
1060 1065 1070

Pro Thr Gly Leu Cys Leu Asn Thr Glu Gly Ser Phe Thr Cys Ser Ala
1075 1080 1085

Cys Gln Ser Gly Tyr Trp Val Asn Glu Asp Gly Thr Ala Cys Glu Asp
1090 1095 1100

Leu Asp Glu Cys Ala Phe Pro Gly Val Cys Pro Thr Gly Val Cys Thr
1105 1110 1115 1120

Asn Thr Val Gly Ser Phe Ser Cys Lys Asp Cys Asp Gln Gly Tyr Arg
1125 1130 1135

Pro Asn Pro Leu Gly Asn Arg Cys Glu Asp Val Asp Glu Cys Glu Gly
1140 1145 1150

Pro Gln Ser Ser Cys Arg Gly Gly Glu Cys Lys Asn Thr Glu Gly Ser
1155 1160 1165

Tyr Gln Cys Leu Cys His Gln Gly Phe Gln Leu Val Asn Gly Thr Met
1170 1175 1180

Cys Glu Asp Val Asn Glu Cys Val Gly Glu Glu His Cys Ala Pro His
1185 1190 1195 1200

Gly Glu Cys Leu Asn Ser Leu Gly Ser Phe Phe Cys Leu Cys Ala Pro
1205 1210 1215

Gly Phe Ala Ser Ala Glu Gly Gly Thr Arg Cys Gln Asp Val Asp Glu
1220 1225 1230

Cys Ala Ala Thr Asp Pro Cys Pro Gly Gly His Cys Val Asn Thr Glu
1235 1240 1245

Gly Ser Phe Ser Cys Leu Cys Glu Thr Ala Ser Phe Gln Pro Ser Pro
1250 1255 1260

Asp Ser Gly Glu Cys Leu Asp Ile Asp Glu Cys Glu Asp Arg Glu Asp
1265 1270 1275 1280

Pro Val Cys Gly Ala Trp Arg Cys Glu Asn Ser Pro Gly Ser Tyr Arg
1285 1290 1295

Cys Ile Leu Asp Cys Gln Pro Gly Phe Tyr Val Ala Pro Asn Gly Asp
1300 1305 1310

Cys Ile Asp Ile Asp Glu Cys Ala Asn Asp Thr Val Cys Gly Asn His
1315 1320 1325

Gly Phe Cys Asp Asn Thr Asp Gly Ser Phe Arg Cys Leu Cys Asp Gln
1330 1335 1340

Gly Phe Glu Thr Ser Pro Ser Gly Trp Glu Cys Val Asp Val Asn Glu
1345 1350 1355 1360

Cys Glu Leu Met Met Ala Val Cys Gly Asp Ala Leu Cys Glu Asn Val
1365 1370 1375

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Glu Gly Ser Phe Leu Cys Leu Cys Ala Ser Asp Leu Glu Glu Tyr Asp
1380 1385 1390

Ala Glu Glu Gly His Cys Arg Pro Arg Val Ala Gly Ala Gln Arg Ile
1395 1400 1405

Pro Glu Val Arg Thr Glu Asp Gln Ala Pro Ser Leu Ile Arg Met Glu
1410 1415 1420

Cys Tyr Ser Glu His Asn Gly Gly Pro Pro Cys Ser Gln Ile Leu Gly
1425 1430 1435 1440

Gln Asn Ser Thr Gln Ala Glu Cys Cys Cys Thr Gln Gly Ala Arg Trp
1445 1450 1455

Gly Lys Ala Cys Ala Pro Cys Pro Ser Glu Asp Ser Val Glu Phe Ser
1460 1465 1470

Gln Leu Cys Pro Ser Gly Gln Gly Tyr Ile Pro Val Glu Gly Ala Trp
1475 1480 1485

Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu Cys Val Leu Phe
1490 1495 1500

Gly Pro Ala Leu Cys Gln Asn Gly Arg Cys Ser Asn Ile Val Pro Gly
1505 1510 1515 1520

Tyr Ile Cys Leu Cys Asn Pro Gly Tyr His Tyr Asp Ala Ser Ser Arg
1525 1530 1535

Lys Cys Gln Asp His Asn Glu Cys Gln Asp Leu Ala Cys Glu Asn Gly
1540 1545 1550

Glu Cys Val Asn Gln Glu Gly Ser Phe His Cys Leu Cys Asn Pro Pro
1555 1560 1565

Leu Thr Leu Asp Leu Ser Gly Gln Arg Cys Val Asn Thr Thr Ser Ser
1570 1575 1580

Thr Glu Asp Phe Pro Asp His Asp Ile His Met Asp Ile Cys Trp Lys
1585 1590 1595 1600

Lys Val Thr Asn Asp Val Cys Ser Gln Pro Leu Arg Gly His His Thr
1605 1610 1615

Thr Tyr Thr Glu Cys Cys Cys Gln Asp Gly Glu Ala Trp Ser Gln Gln
1620 1625 1630

Cys Ala Leu Cys Pro Pro Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys
1635 1640 1645

Asn Val Ala Arg Ile Glu Ala Glu Arg Gly Ala Gly Ile His Phe Arg
1650 1655 1660

Pro Gly Tyr Glu Tyr Gly Pro Gly Leu Asp Asp Leu Pro Glu Asn Leu
1665 1670 1675 1680

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Tyr Gly Pro Asp Gly Ala Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp
1685 1690 1695

Thr Ala Pro Glu Pro Pro Phe Ser Asn Pro Ala Ser Gln Pro Gly Asp
1700 1705 1710

Asn Thr Pro Val Leu Glu Pro Pro Leu Gln Pro Ser Glu Leu Gln Pro
1715 1720 1725

His Tyr Leu Ala Ser His Ser Glu Pro Pro Ala Ser Phe Glu Gly Leu
1730 1735 1740

Gln Ala Glu Glu Cys Gly Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys
1745 1750 1755 1760

Val Arg Val Arg Glu Gly Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln
1765 1770 1775

Leu Asp Ala Pro Thr Leu Ala Cys Val Asp Val Asn Glu Cys Glu Asp
1780 1785 1790

Leu Asn Gly Pro Ala Arg Leu Cys Ala His Gly His Cys Glu Asn Thr
1795 1800 1805

Glu Gly Ser Tyr Arg Cys His Cys Ser Pro Gly Tyr Val Ala Glu Pro
1810 1815 1820

Gly Pro Pro His Cys Ala Ala Lys Glu
1825 1830

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG CGC CAG GCC GGC GGA TTG GGG CTG CTG GCA CTA CTC CTG CTG GCG	48
Met Arg Gln Ala Gly Gly Leu Gly Leu Leu Ala Leu Leu Leu Ala	15
1 5 10	
CTG CTG GGC CCC GGC GGC CGA GGG GTG GGC CGG CCG GGC AGC GGG GCA	96
Leu Leu Gly Pro Gly Gly Arg Gly Val Gly Arg Pro Gly Ser Gly Ala	30
20 25 30	
CAG GCG GGG GCG GGC CGC TGG GCC CAA CGC TTC AAG GTG GTC TTT GCG	144
Gln Ala Gly Ala Gly Arg Trp Ala Gln Arg Phe Lys Val Val Phe Ala	45
35 40 45	

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CCT GTG ATC TGC AAG CGG ACC TGT CTG AAG GGC CAG TGT CGG GAC AGC	192
Pro Val Ile Cys Lys Arg Thr Cys Leu Lys Gly Gln Cys Arg Asp Ser	
50 55 60	
TGT CAG CAG GGC TCC AAC ATG ACG CTC ATC GGA GAG AAC GGC CAC AGC	240
Cys Gln Gln Gly Ser Asn Met Thr Leu Ile Gly Glu Asn Gly His Ser	
65 70 75 80	
ACC GAC ACG CTC ACC GGT TCT GCC TTC CGC GTG GTG GTG TGC CCT CTA	288
Thr Asp Thr Leu Thr Gly Ser Ala Phe Arg Val Val Val Cys Pro Leu	
85 90 95	
CCC TGC ATG AAC GGT GGC CAG TGC TCT TCC CGA AAC CAG TGC CTG TGT	336
Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asn Gln Cys Leu Cys	
100 105 110	
CCC CCG GAT TTC ACG GGG CGC TTC TGC CAG GTG CCT GCT GCA GGA ACC	384
Pro Pro Asp Phe Thr Gly Arg Phe Cys Gln Val Pro Ala Ala Gly Thr	
115 120 125	
GGA GCT GGC ACC GGG AGT TCA GGC CCC GGC TGG CCC GAC CGG GCC ATG	432
Gly Ala Gly Thr Gly Ser Ser Gly Pro Gly Trp Pro Asp Arg Ala Met	
130 135 140	
TCC ACA GGC CCG CTG CCG CCC CTT GCC CCA GAA GGA GAG TCT GTG GCT	480
Ser Thr Gly Pro Leu Pro Pro Leu Ala Pro Glu Gly Glu Ser Val Ala	
145 150 155 160	
AGC AAA CAC GCC ATT TAC GCG GTG CAG GTG ATC GCA GAT CCT CCC GGG	528
Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala Asp Pro Pro Gly	
165 170 175	
CCG GGG GAG GGT CCT CCT GCA CAA CAT GCA GCC TTC TTG GTG CCC CTG	576
Pro Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe Leu Val Pro Leu	
180 185 190	
GGG CCA GGA CAA ATC TCG GCA GAA GTG CAG GCT CCG CCC CCC GTG GTG	624
Gly Pro Gly Gln Ile Ser Ala Glu Val Gln Ala Pro Pro Pro Val Val	
195 200 205	
AAC GTG CGT GTC CAT CAC CCT CCT GAA GCT TCC GTT CAG GTG CAC CGC	672
Asn Val Arg Val His His Pro Pro Glu Ala Ser Val Gln Val His Arg	
210 215 220	
ATC GAG GGG CCG AAC GCT GAA GGC CCA GCC TCT TCC CAG CAC TTG CTG	720
Ile Glu Gly Pro Asn Ala Glu Gly Pro Ala Ser Ser Gln His Leu Leu	
225 230 235 240	
CCG CAT CCC AAG CCC CCG CAC CCG AGG CCA CCC ACT CAA AAG CCA CTG	768
Pro His Pro Lys Pro Pro His Pro Arg Pro Pro Thr Gln Lys Pro Leu	
245 250 255	
GGC CGC TGC TTC CAG GAC ACA TTG CCC AAG CAG CCT TGT GGC AGC AAC	816
Gly Arg Cys Phe Gln Asp Thr Leu Pro Lys Gln Pro Cys Gly Ser Asn	
260 265 270	

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CCT TTG CCT GGC CTT ACC AAG CAG GAA GAT TGC TGC GGT AGC ATC GGT Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile Gly 275 280 285	864
ACT GCC TGG GGA CAA AGC AAG TGT CAC AAG TGC CCA CAG CTT CAG TAT Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr 290 295 300	912
ACA GGG GTG CAG AAG CCT GTA CCT GTA CGT GGG GAG GTG GGT GCT GAC Thr Gly Val Lys Pro Val Pro Val Arg Gly Glu Val Gly Ala Asp 305 310 315 320	960
TGC CCC CAG GGC TAC AAG AGG CTC AAC AGC ACC CAC TGC CAG GAT ATC Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr His Cys Gln Asp Ile 325 330 335	1008
AAC GAA TGT GCG ATG CCC GGG AAT GTG TGC CAT GGT GAC TGC CTC AAC Asn Glu Cys Ala Met Pro Gly Asn Val Cys His Gly Asp Cys Leu Asn 340 345 350	1056
AAC CCT GGC TCT TAT CGC TGT GTC TGC CCG CCC GGT CAT AGC TTG GGT Asn Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly 355 360 365	1104
CCC CTC GCA GCA CAG TGC ATT GCC GAC AAA CCA GAG GAG AAG AGC CTG Pro Leu Ala Ala Gln Cys Ile Ala Asp Lys Pro Glu Glu Lys Ser Leu 370 375 380	1152
TGT TTC CGC CTT GTG AGC ACC GAA CAC CAG TGC CAG CAC CCT CTG ACC Cys Phe Arg Leu Val Ser Thr Glu His Gln Cys Gln His Pro Leu Thr 385 390 395 400	1200
ACA CGC CTA ACC CGC CAG CTC TGC TGC TGT AGT GTG GGT AAA GCC TGG Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp 405 410 415	1248
GGT GCC CGG TGC CAG CGC TGC CCG GCA GAT GGT ACA GCA GCC TTC AAG Gly Ala Arg Cys Gln Arg Cys Pro Ala Asp Gly Thr Ala Ala Phe Lys 420 425 430	1296
GAG ATC TGC CCC GGC TGG GAA AGG GTA CCA TAT CCT CAC CTC CCA CCA Glu Ile Cys Pro Gly Trp Glu Arg Val Pro Tyr Pro His Leu Pro Pro 435 440 445	1344
GAC GCT CAC CAT CCA GGG GGA AAG CGA CTT CTC CCT CTT CCT GCA CCC Asp Ala His His Pro Gly Gly Lys Arg Leu Leu Pro Leu Pro Ala Pro 450 455 460	1392
GAC GGG CCA CCC AAA CCC CAG CAG CTT CCT GAA AGC CCC AGC CGA GCA Asp Gly Pro Pro Lys Pro Gln Gln Leu Pro Glu Ser Pro Ser Arg Ala 465 470 475 480	1440
CCA CCC CTC GAG GAC ACA GAG GAA GAG AGA GGA GTG ACC ATG GAT CCA Pro Pro Leu Glu Asp Thr Glu Glu Glu Arg Gly Val Thr Met Asp Pro 485 490 495	1488
CCA GTG AGT GAG GAG CGA TCG GTG CAG CAG AGC CAC CCC ACT ACC ACC	1536

Pro	Val	Ser	Glu	Glu	Arg	Ser	Val	Gln	Gln	Ser	His	Pro	Thr	Thr	Thr		
			500				505						510				
ACC Thr	TCA Ser	CCC Pro	CCC Pro	CGG Arg	CCT Pro	TAC Tyr	CCA Pro	GAG Glu	CTC Leu	ATC Ile	TCT Ser	CGC Arg	CCC Pro	TCC Ser	CCA Pro	1584	
			515				520				525						
CCT Pro	ACC Thr	TTC Phe	CAC His	CGG Arg	TTC Phe	CTG Leu	CCA Pro	GAC Asp	TTG Leu	CCC Pro	CCA Pro	TCC Ser	CGA Arg	AGT Ser	GCA Ala	1632	
			530				535				540						
GTG Val	GAG Glu	ATC Ile	GCC Ala	JCC Pro	ACT Thr	CAG Gln	GTC Val	ACA Thr	GAG Glu	ACC Thr	GAT Asp	GAG Glu	TGC Cys	CGA Arg	TTG Leu	1680	
			545				550				555						
AAC Asn	CAG Gln	AAT Asn	ATC Ile	TGT Cys	GGC Gly	CAT His	GGA Gly	CAG Gln	TGT Cys	GTG Val	CCT Pro	GGC Gly	CCC Pro	TCG Ser	GAT Asp	1728	
			565				570				575						
TAC Tyr	TCC Ser	TGC Cys	CAC His	TGC Cys	AAC Asn	GCT Ala	GGC Gly	TAC Tyr	CGG Arg	TCA Ser	CAC His	CCG Pro	CAG Gln	CAC His	CGC Arg	1776	
			580				585				590						
TAC Tyr	TGT Cys	GTT Val	GAT Asp	GTG Val	AAC Asn	GAG Glu	TGC Cys	GAG Glu	GCA Ala	GAG Glu	CCC Pro	TGC Cys	GGC Gly	CCC Pro	GGG Gly	1824	
			595				600				605						
AAA Lys	GGC Gly	ATC Ile	TGT Cys	ATG Met	AAC Asn	ACT Thr	GGT Gly	GGC Gly	TCC Ser	TAC Tyr	AAT Asn	TGT Cys	CAC His	TGC Cys	AAC Asn	1872	
			610				615				620						
CGA Arg	GGC Gly	TAC Tyr	CGC Arg	CTC Leu	CAC His	GTG Val	GGT Gly	GCA Ala	GGG Gly	GGC Gly	CGC Arg	TCG Ser	TGC Cys	GTG Val	GAC Asp	1920	
			625				630				635						
CTG Leu	AAC Asn	GAG Glu	TGC Cys	GCC Ala	AAG Lys	CCT Pro	CAC His	CTG Leu	TGT Cys	GGG Gly	GAC Asp	GGT Gly	GGC Gly	TTC Phe	TGC Cys	1968	
			645				650				655						
ATC Ile	AAC Asn	TTC Phe	CCT Pro	GGT Gly	CAC His	TAC Tyr	AAA Lys	TGC Cys	AAC Asn	TGC Cys	TAT Tyr	CCT Pro	GGC Gly	TAC Tyr	CGG Arg	2016	
			660				665				670						
CTC Leu	AAG Lys	GCC Ala	TCC Ser	CGA Arg	CCG Pro	CCC Pro	ATT Ile	TGC Cys	GAA Glu	GAC Asp	ATC Ile	GAC Asp	GAG Glu	TGT Cys	CGC Arg	2064	
			675				680				685						
GAC Asp	CCT Pro	AGC Ser	ACC Thr	TGC Cys	CCT Pro	GAT Asp	GGC Gly	AAA Lys	TGT Cys	GAA Glu	AAC Asn	AAA Lys	CCT Pro	GGC Gly	AGC Ser	2112	
			690				695				700						
TTC Phe	AAG Lys	TGC Cys	ATC Ile	GCC Ala	TGC Cys	CAG Gln	CCT Pro	GGC Gly	TAC Tyr	CGT Arg	AGC Ser	CAG Gln	GGG Gly	GGC Gly	GGG Gly	2160	
			705				710				715						
GCC Ala	TGT Cys	CGT Arg	GAT Asp	GTC Val	AAC Asn	GAA Glu	TGC Cys	TCC Ser	GAG Glu	GGT Gly	ACC Thr	CCC Pro	TGC Cys	TCT Ser	CCT Pro	2208	
			720														

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725										730					735					
GGA	TGG	TGT	GAG	AAC	CTT	CCG	GGT	TCT	TAC	CGT	TGC	ACG	TGT	GCC	CAG	2256				
Gly	Trp	Cys	Glu	Asn	Leu	Pro	Gly	Ser	Tyr	Arg	Cys	Thr	Cys	Ala	Gln					
			740			745			750											
GGG	ATA	CGA	ACC	CGC	ACA	GGA	CGC	CTC	AGT	TGC	ATA	GAC	GTG	GAT	GAG	2304				
Gly	Ile	Arg	Thr	Arg	Thr	Gly	Arg	Leu	Ser	Cys	Ile	Asp	Val	Asp	Glu					
			755			760			765											
TGT	GAG	GCT	GGG	AAA	GTG	TGC	CAA	GAT	GGC	ATC	TGC	ACG	AAC	ACA	CCA	2352				
Cys	Glu	Ala	Gly	Lys	Val	Cys	Gln	Asp	Gly	Ile	Cys	Thr	Asn	Thr	Pro					
			770			775			780											
GGC	TCT	TTC	CAG	TGT	CAG	TGC	CTC	TCC	GGC	TAT	CAT	CTG	TCA	AGG	GAT	2400				
Gly	Ser	Phe	Gln	Cys	Gln	Cys	Leu	Ser	Gly	Tyr	His	Leu	Ser	Arg	Asp					
			785			790			795			800								
CGG	AGC	CGC	TGT	GAG	GAC	ATT	GAT	GAA	TGT	GAC	TTC	CCT	GCG	GCC	TGC	2448				
Arg	Ser	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Asp	Phe	Pro	Ala	Ala	Cys					
			805			810			815											
ATC	GGG	GGT	GAC	TGC	ATC	AAT	ACC	AAT	GGT	TCC	TAC	AGA	TGT	CTC	TGT	2496				
Ile	Gly	Gly	Asp	Cys	Ile	Asn	Thr	Asn	Gly	Ser	Tyr	Arg	Cys	Leu	Cys					
			820			825			830											
CCC	CTG	GGT	CAT	CGG	TTG	GTG	GGC	GGC	AGG	AAG	TGC	AAG	AAA	GAT	ATA	2544				
Pro	Leu	Gly	His	Arg	Leu	Val	Gly	Gly	Arg	Lys	Cys	Lys	Lys	Asp	Ile					
			835			840			845											
GAT	GAG	TGC	AGC	CAG	GAC	CCA	GGC	CTG	TGC	CTG	CCC	CAT	GCC	TGC	GAG	2592				
Asp	Glu	Cys	Ser	Gln	Asp	Pro	Gly	Leu	Cys	Leu	Pro	His	Ala	Cys	Glu					
			850			855			860											
AAC	CTC	CAG	GGC	TCC	TAT	GTC	TGT	GTC	TGT	GAT	GAG	GGT	TTC	ACA	CTC	2640				
Asn	Leu	Gln	Gly	Ser	Tyr	Val	Cys	Val	Cys	Asp	Glu	Gly	Phe	Thr	Leu					
			865			870			875			880								
ACC	CAG	GAC	CAG	CAT	GGG	TGT	GAG	GAG	GTG	GAG	CAG	CCC	CAC	CAC	AAG	2688				
Thr	Gln	Asp	Gln	His	Gly	Cys	Glu	Glu	Val	Glu	Gln	Pro	His	His	Lys					
			885			890			895											
AAG	GAG	TGC	TAC	CTT	AAC	TTC	GAT	GAC	ACA	GTG	TTC	TGT	GAC	AGC	GTA	2736				
Lys	Glu	Cys	Tyr	Leu	Asn	Phe	Asp	Asp	Thr	Val	Phe	Cys	Asp	Ser	Val					
			900			905			910											
TTG	GCT	ACC	AAT	GTC	ACT	CAG	CAG	GAA	TGC	TGT	TGC	TCT	CTG	GGA	GCT	2784				
Leu	Ala	Thr	Asn	Val	Thr	Gln	Gln	Glu	Cys	Cys	Cys	Ser	Leu	Gly	Ala					
			915			920			925											
GGC	TGG	GGA	GAC	CAC	TGC	GAA	ATC	TAT	CCC	TGT	CCA	GTC	TAC	AGC	TCA	2832				
Gly	Trp	Gly	Asp	His	Cys	Glu	Ile	Tyr	Pro	Cys	Pro	Val	Tyr	Ser	Ser					
			930			935			940											
GCC	GAA	TTT	CAC	AGC	CTG	GTG	CCT	GAT	GGG	AAA	AGG	CTA	CAC	TCA	GGA	2880				
Ala	Glu	Phe	His	Ser	Leu	Val	Pro	Asp	Gly	Lys	Arg	Leu	His	Ser	Gly					
			945			950			955			960								

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CAA CAA CAT TGT GAA CTA TGC ATT CCT GCC CAC CGT GAC ATC GAC GAA Gln Gln His Cys Glu Leu Cys Ile Pro Ala His Arg Asp Ile Asp Glu 965 970 975	2928
TGC ATA TTG TTT GGG GCA GAG ATC TGC AAG GAG GGC AAG TGT GTG AAC Cys Ile Leu Phe Gly Ala Glu Ile Cys Lys Glu Gly Lys Cys Val Asn 980 985 990	2976
ACG CAG CCC GGC TAC GAG TGC TAC TCC AAG CAG GGC TTC TAC TAC GAT Thr Gln Pro Gly Tyr Glu Cys Tyr Cys Lys Gln Gly Phe Tyr Tyr Asp 995 1000 1005	3024
GGC AAC CTG CTG GAG TGC GTG GAC GTG GAT GAG TGC TTG GAT GAG TCT Gly Asn Leu Leu Glu Cys Val Asp Val Asp Glu Cys Leu Asp Glu Ser 1010 1015 1020	3072
AAC TGC AGG AAC GGA GTG TGT GAG AAC ACA CGT GGC GGC TAC CGC TGT Asn Cys Arg Asn Gly Val Cys Glu Asn Thr Arg Gly Gly Tyr Arg Cys 1025 1030 1035 1040	3120
GCC TGC ACT CCG CCG GCA GAG TAC AGT CCC GCA CAG GCC CAG TGT CTG Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln Ala Gln Cys Leu 1045 1050 1055	3168
ATC CCG GAG AGA TGG AGC ACG CCC CAG AGA GAC GTG AAG TGT GCT GGG Ile Pro Glu Arg Trp Ser Thr Pro Gln Arg Asp Val Lys Cys Ala Gly 1060 1065 1070	3216
GCC AGC GAG GAG AGG ACG GCA TGT GTA TGG GGC CCC TGG GCG GGA CCT Ala Ser Glu Glu Arg Thr Ala Cys Val Trp Gly Pro Trp Ala Gly Pro 1075 1080 1085	3264
GCC CTC ACT TTT GAT GAC TGC TGC TGC CGC CAG CCG CGG CTG GGT ACC Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Pro Arg Leu Gly Thr 1090 1095 1100	3312
CAG TGC AGA CCG TGC CCG CCA CGT GGC ACC GGG TCC CAG TGC CCG ACT Gln Cys Arg Pro Cys Pro Pro Arg Gly Thr Gly Ser Gln Cys Pro Thr 1105 1110 1115 1120	3360
TCA CAG AGT GAG AGC AAT TCT TTC TGG GAC ACA AGC CCC CTG CTA CTG Ser Gln Ser Glu Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu 1125 1130 1135	3408
GGG AAG TCT CCG CGA GAC GAA GAC AGC TCA GAG GAG GAT TCA GAT GAG Gly Lys Ser Pro Arg Asp Glu Asp Ser Ser Glu Glu Asp Ser Asp Glu 1140 1145 1150	3456
TGC CGT TGT GTG AGC GGA CGC TGT GTG CCA CGG CCA GGC GGG GCG GTA Cys Arg Cys Val Ser Gly Arg Cys Val Pro Arg Pro Gly Gly Ala Val 1155 1160 1165	3504
TGC GAG TGT CCT GGA GGC TTT CAG CTG GAC GCC TCC CGT GCC CGC TGC Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys 1170 1175 1180	3552

GTG GAC ATT GAT GAG TGC CGA GAA CTG AAC CAG CGG GGA CTG CTG TGT	3600
Val Asp Ile Asp Glu Cys Arg Glu Leu Asn Gln Arg Gly Leu Leu Cys	
1185 1190 1195 1200	
AAG AGC GAG CGG TGC GTG AAC ACC AGT GGA TCC TTC CCG TGT GTC TGC	3648
Lys Ser Glu Arg Cys Val Asn Thr Ser Gly Ser Phe Arg Cys Val Cys	
1205 1210 1215	
AAA GCT GGC TTC ACG CGC AGC CGC CCT CAC GGG CCT GCG TGC CTC AGC	3696
Lys Ala Gly Phe Thr Arg Ser Arg Pro His Gly Pro Ala Cys Leu Ser	
1220 1225 1230	
GCC GCC GCT GAT GAT GCA GCC ATA GCC CAC ACC TCA GTG ATC GAT CAT	3744
Ala Ala Ala Asp Asp Ala Ala Ile Ala His Thr Ser Val Ile Asp His	
1235 1240 1245	
CGA GGG TAT TTT CAC	3759
Arg Gly Tyr Phe His	
1250	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Gln	Ala	Gly	Gly	Leu	Gly	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Ala	15
1				5				10								
Leu	Leu	Gly	Pro	Gly	Gly	Arg	Gly	Val	Gly	Arg	Pro	Gly	Ser	Gly	Ala	30
			20					25								
Gln	Ala	Gly	Ala	Gly	Arg	Trp	Ala	Gln	Arg	Phe	Lys	Val	Val	Phe	Ala	45
			35				40									
Pro	Val	Ile	Cys	Lys	Arg	Thr	Cys	Leu	Lys	Gly	Gln	Cys	Arg	Asp	Ser	60
			50				55									
Cys	Gln	Gln	Gly	Ser	Asn	Met	Thr	Leu	Ile	Gly	Glu	Asn	Gly	His	Ser	80
			65			70				75						
Thr	Asp	Thr	Leu	Thr	Gly	Ser	Ala	Phe	Arg	Val	Val	Val	Cys	Pro	Leu	95
				85					90							
Pro	Cys	Met	Asn	Gly	Gly	Gln	Cys	Ser	Ser	Arg	Asn	Gln	Cys	Leu	Cys	110
				100				105								
Pro	Pro	Asp	Phe	Thr	Gly	Arg	Phe	Cys	Gln	Val	Pro	Ala	Ala	Gly	Thr	125
				115			120									
Gly	Ala	Gly	Thr	Gly	Ser	Ser	Gly	Pro	Gly	Trp	Pro	Asp	Arg	Ala	Met	

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130

135

140

Ser Thr Gly Pro Leu Pro Pro Leu Ala Pro Glu Gly Glu Ser Val Ala
145 150 155 160

Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala Asp Pro Pro Gly
165 170 175

Pro Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe Leu Val Pro Leu
180 185 190

Gly Pro Gly Gln Ile Ser Ala Glu Val Gln Ala Pro Pro Pro Val Val
195 200 205

Asn Val Arg Val His His Pro Pro Glu Ala Ser Val Gln Val His Arg
210 215 220

Ile Glu Gly Pro Asn Ala Glu Gly Pro Ala Ser Ser Gln His Leu Leu
225 230 235 240

Pro His Pro Lys Pro Pro His Pro Arg Pro Pro Thr Gln Lys Pro Leu
245 250 255

Gly Arg Cys Phe Gln Asp Thr Leu Pro Lys Gln Pro Cys Gly Ser Asn
260 265 270

Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile Gly
275 280 285

Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr
290 295 300

Thr Gly Val Gln Lys Pro Val Pro Val Arg Gly Glu Val Gly Ala Asp
305 310 315 320

Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr His Cys Gln Asp Ile
325 330 335

Asn Glu Cys Ala Met Pro Gly Asn Val Cys His Gly Asp Cys Leu Asn
340 345 350

Asn Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly
355 360 365

Pro Leu Ala Ala Gln Cys Ile Ala Asp Lys Pro Glu Glu Lys Ser Leu
370 375 380

Cys Phe Arg Leu Val Ser Thr Glu His Gln Cys Gln His Pro Leu Thr
385 390 395 400

Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp
405 410 415

Gly Ala Arg Cys Gln Arg Cys Pro Ala Asp Gly Thr Ala Ala Phe Lys
420 425 430

Glu Ile Cys Pro Gly Trp Glu Arg Val Pro Tyr Pro His Leu Pro Pro

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445

SECRET

750

Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln Ala Gln Cys Leu

SECRET

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1045	1050	1055
Ile Pro Glu Arg Trp Ser Thr Pro Gln Arg Asp Val Lys Cys Ala Gly 1060 1065 1070		
Ala Ser Glu Glu Arg Thr Ala Cys Val Trp Gly Pro Trp Ala Gly Pro 1075 1080 1085		
Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Pro Arg Leu Gly Thr 1090 1095 1100		
Gln Cys Arg Pro Cys Pro Phe Arg Gly Thr Gly Ser Gln Cys Pro Thr 1105 1110 1115 1120		
Ser Gln Ser Glu Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu 1125 1130 1135		
Gly Lys Ser Pro Arg Asp Glu Asp Ser Ser Glu Glu Asp Ser Asp Glu 1140 1145 1150		
Cys Arg Cys Val Ser Gly Arg Cys Val Pro Arg Pro Gly Gly Ala Val 1155 1160 1165		
Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys 1170 1175 1180		
Val Asp Ile Asp Glu Cys Arg Glu Leu Asn Gln Arg Gly Leu Leu Cys 1185 1190 1195 1200		
Lys Ser Glu Arg Cys Val Asn Thr Ser Gly Ser Phe Arg Cys Val Cys 1205 1210 1215		
Lys Ala Gly Phe Thr Arg Ser Arg Pro His Gly Pro Ala Cys Leu Ser 1220 1225 1230		
Ala Ala Ala Asp Asp Ala Ala Ile Ala His Thr Ser Val Ile Asp His 1235 1240 1245		
Arg Gly Tyr Phe His 1250		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Glu	Ser	Val	Ala	Ser	Lys	His	Ala	Ile	Tyr	Ala	Val	Cys
1					5				10				

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACCGATGCT ACCGCAGCAA TCTT

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGCCTAAAC TCTACCAGCA CG

22

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCACGTC ATCCATTCCA CA

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGTCCAAGTT GTGTCTTAGC AG

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro Leu Gly Pro Lys Gly
1 5 10 15
Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys Gly Glu Gln Gly Pro
20 25 30
Lys Gly Glu Thr Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Pro Ala
35 40 45
Gly Glu Glu Gly Lys
50

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCCTCCCG GTCCTCAAGG TGCAACTGGT CCTCTGGGCC CCAAAGGTCA GACGGGTGAG 60
CCCGGCATCG CTGGCTTCAA AGGTGAACAA GGCCCCAAGG GAGAGACTGG ACCTGCTGGG 120
CCCCAGGGAG CCCCTGGCCC TGCTGGTGAA GAAGGAAAA 159

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "N = A or G or C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAACGTCACA CGTGANACGT GAACGTTGCT TGCTGG 36

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid

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86

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTACGTCCAC GTACACGTCT AGCAAGCAAG CA

32

002790" 58926560